9.0 CALCULATION OF DATA QUALITY INDICATORS

As discussed in Section 3.2, in order to ensure high quality and defensible data, data quality indicators will be measured during offsite chemical analysis. Calculation of these data quality indicators is presented below.

9.1 PRECISION

According to EM 200-1-3 (USACE 2001):

Precision refers to the distribution of a set of reported values about the mean, or the closeness of agreement between individual test results obtained under prescribed conditions. Precision reflects the random error and may be affected by systematic error. Precision also characterizes the natural variation of the matrix and how the contamination exists or varies within that matrix. Precision is evaluated using analyses of an analytical sample and its corresponding matrix duplicate and/or laboratory matrix spike/matrix spike duplicate, which not only exhibit sampling precision, but indicate analytical precision through the reproducibility of the analytical results. Precision determined by RPD shall be calculated as follows:

$$RPD = \frac{(X_1 - X_2)}{\left[\left(\frac{X_1 - X_2}{2}\right)\right]} x100$$

where:

X_1 = *Measured value of sample or matrix spike*

X_2 = *Measured value of duplicate or matrix spike duplicate*

9.2 ACCURACY

Analytical accuracy may be assessed through the use of known and unknown QC samples and spiked samples. Accuracy is presented as percent recovery. Accuracy will be determined from matrix spike, matrix spike duplicate, and laboratory control samples, as well as from surrogate compounds added to organic fractions and is calculated as follows:

$$Accuracy(\%R) = \frac{(X_s - X_u)}{K} x100$$

REVISED DRAFT

O:\25692709 USACE\53-F0072173.00 Brdford1\Delivery Order No. 04 Mod 06\Work Plans - Draft\QAPP\QAPP Revised Draft\QAPP Revised Draft.doc   9-1

where:

         Xs   - Measured value of the spike sample

         Xu   - Measured value of the unspiked sample

         K   - Known amount of spike in the sample

9.3   COMPLETENESS

Completeness is calculated on a per matrix basis for the project and is calculated as follows:

$$Completeness\,(\%\,C) = \frac{(X_y - X_n)}{N} x100$$

where:

         Xv - Number of valid measurements

         Xn - Number of invalid measurements

         N   - Number of valid measurements expected to be obtained

9.4   METHOD DETECTION LIMITS (MDLS)

MDLs shall be determined for each target analyte using procedures outlined in 40 CFR Part 136, Appendix B. The method detection limit normally is calculated using data generated from reagent water. MDLs are calculated as follows:

$$MDL \;\; = \;\; t_{(n-1,\,1-\mu\,=\,0.99)}\,(S)$$

where: $t_{(n-1,\,1-\mu\,=\,0.99)} =$ Student's t-value appropriate to a 99% confidence level and a standard deviation estimate with n-1 degrees of freedom

                     $S =$ Standard deviation of the replicate analyses

REVISED DRAFT

URS   O:\25692709 USACE\53-F0072173.00 Brdford1\Delivery Order No. 04 Mod 06\Work Plans - Draft\QAPP\QAPP Revised Draft\QAPP Revised Draft.doc   9-2